

## Sequence listing

IAP12 Rec'd PCT/PTO 11 MAY 2006

&lt;110&gt; Vollmers, Philip

&lt;120&gt; Human monoclonal antibody

&lt;150&gt; DE-10 353 175.0

&lt;151&gt; 2003-11-14

&lt;160&gt; 4

&lt;210&gt; 1

&lt;211&gt; 96

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Amino acid sequence of the variable region of the light chain (V<sub>L</sub>) of antibody SAM-6

&lt;400&gt; 1

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly  
1 5 10 15

Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys  
20 25 30

Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu  
35 40 45

Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg  
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser  
65 70 75

Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp  
80 85 90

Asp Ser Ser Ile Val Val  
95

**REPLACEMENT (RULE 26)**

&lt;210&gt; 2

&lt;211&gt; 288

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence of the variable region of the light chain (V<sub>L</sub>) of antibody SAM-6

&lt;400&gt; 2

tcc	tat	gtg	ctg	act	cag	cca	ccc	tca	gtg	tcc	gtg	tcc	cca	gga	45
Ser	Tyr	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ser	Pro	Gly	
1				5				10						15	

## CDR1

cag	aca	gcc	agc	atc	acc	tgc	tct	gga	gat	aaa	ttg	ggg	gat	aaa	90
Gln	Thr	Ala	Ser	Ile	Thr	Cys	Ser	Gly	Asp	Lys	Leu	Gly	Asp	Lys	
			20					25						30	

tat	gct	tgc	tgg	tat	cag	cag	aag	cca	ggc	cag	tcc	cct	gtg	ctg	135
Tyr	Ala	Cys	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Val	Leu	
			35					40						45	

## CDR2

gtc	atc	tat	caa	gat	agc	aag	cgg	ccc	tca	ggg	atc	cct	gag	cga	180
Val	Ile	Tyr	Gln	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
			50					55						60	

ttc	tct	ggc	tcc	aac	tct	ggg	aac	aca	gcc	act	ctg	acc	atc	agc	225
Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	
			65					70						75	

ggg	acc	cag	gct	atg	gat	gag	gct	gac	tat	tac	tgt	cag	gcg	tgg	270
Gly	Thr	Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp	
			80					85						90	

## CDR3

gac	agc	agc	att	gtg	gta	288
Asp	Ser	Ser	Ile	Val	Val	
			95			

**REPLACEMENT (RULE 26)**

&lt;210&gt; 3

&lt;211&gt; 110

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Amino acid sequence of the variable region of the heavy chain (V<sub>H</sub>) of antibody SAM-6

&lt;400&gt; 3

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly  
1 5 10 15

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
20 25 30

Ser Tyr Ala Met His Trp Val Arg Glu Ala Pro Gly Lys Gly Leu  
35 40 45

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr  
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser  
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp  
80 85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly  
95 100 105

Lys Thr Phe Asp Tyr  
110

**REPLACEMENT (RULE 26)**

&lt;210&gt; 4

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Nucleotide sequence of the variable region of the heavy chain (V<sub>H</sub>) of antibody SAM-6

&lt;400&gt; 4

cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	cct	ggg	45
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	
1				5					10					15	

agg	tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	agt	90
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
				20					25					30	

**CDR1**

agc	tat	gct	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	135
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Glu	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	

**CDR2**

gag	tgg	gtg	gca	ggt	ata	tca	tat	gat	gga	agc	aat	aaa	tac	tac	180
Glu	Trp	Val	Ala	Val	Ile	Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	
				50					55					60	

gca	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	225
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
				65					70					75	

aag	aac	acg	ctg	tat	ctg	caa	atg	aac	agc	ctg	aga	gct	gag	gac	270
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	

**CDR3**

acg	gct	gtg	tat	tac	tgt	gcg	aga	gat	cgg	tta	gca	gtg	gct	ggt	315
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Leu	Ala	Val	Ala	Gly	
				95					100					105	

aaa	act	ttt	gac	tac											
Lys	Thr	Phe	Asp	Tyr											
															110

**REPLACEMENT (RULE 26)**